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RAW SEQUENCE LISTING

DATE: 08/18/2004

PATENT APPLICATION: US/09/931,701A

TIME: 12:33:20

Input Set : N:\DA\US09931701A.raw

Output Set: N:\CRF4\08102004\I931701A.raw

1 <110> APPLICANT: Outtrup, Helle
2 Pedersen, Poul
3 Sorensen, Marianne
4 <120> TITLE OF INVENTION: Subtilase Enzymes
5 <130> FILE REFERENCE: 10065.200-US
C--> 6 <140> CURRENT APPLICATION NUMBER: US/09/931,701A
7 <141> CURRENT FILING DATE: 2001-08-16
8 <160> NUMBER OF SEQ ID NOS: 9
9 <170> SOFTWARE: PatentIn version 3.1
11 <210> SEQ ID NO: 1
12 <211> LENGTH: 1143
13 <212> TYPE: DNA
14 <213> ORGANISM: Bacillus clausii
15 <220> FEATURE:
16 <221> NAME/KEY: CDS
17 <222> LOCATION: (1)..(1140)
18 <223> OTHER INFORMATION:
19 <221> NAME/KEY: mat_peptide
20 <222> LOCATION: (334)..()
21 <223> OTHER INFORMATION:

ENTERED

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24 Met Asn Lys Pro Leu Gly Lys Ile Val Ala Ser Thr Ala Leu Leu
25 -110 -105 -100
26 att tct gtc gct ttt agt tca tcg att gca tcg gct gct gaa gaa gca 93
27 Ile Ser Val Ala Phe Ser Ser Ile Ala Ser Ala Glu Glu Ala
28 -95 -90 -85
29 aaa gaa aaa tac tta att ggc ttt aat gaa cag gaa gct gtc agt gag 141
30 Lys Glu Lys Tyr Leu Ile Gly Phe Asn Glu Gln Glu Ala Val Ser Glu
31 -80 -75 -70 -65
32 ttt gtc gaa caa gta gat gca aat aat gat gtc gcc gtt ctc tct gag 189
33 Phe Val Glu Gln Val Asp Ala Asn Asn Asp Val Ala Val Leu Ser Glu
34 -60 -55 -50
35 gaa gag gaa gtc gaa att gaa ctg ctt cat gag ttc gaa acc att ccc 237
36 Glu Glu Glu Val Glu Ile Glu Leu Leu His Glu Phe Glu Thr Ile Pro
37 -45 -40 -35
38 gtt tta tca gta gag tta agc cca gaa gat gtg gat acg ctt gaa ctc 285
39 Val Leu Ser Val Glu Leu Ser Pro Glu Asp Val Asp Thr Leu Glu Leu
40 -30 -25 -20
41 gat cca gcg att tct tac att gag gaa gat gta gaa gta tcg att atg 333
42 Asp Pro Ala Ile Ser Tyr Ile Glu Glu Asp Val Glu Val Ser Ile Met
43 -15 -10 -5 -1
44 gct cag tct gtg cca tgg gga att agc cgt gtg caa gca cct gcc gcc 381

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| | | |
|----|---|------|
| 45 | Ala Gln Ser Val Pro Trp Gly Ile Ser Arg Val Gln Ala Pro Ala Ala | |
| 46 | 1 5 10 15 | |
| 47 | cat aac cgc gga gtg aca ggt tcc ggt gta aaa gtt gct gtt ctt gat | 429 |
| 48 | His Asn Arg Gly Val Thr Gly Ser Gly Val Lys Val Ala Val Leu Asp | |
| 49 | 20 25 30 | |
| 50 | aca ggc att tcc gcc cat cca gac tta aat atc cgc ggc ggt gct agc | 477 |
| 51 | Thr Gly Ile Ser Ala His Pro Asp Leu Asn Ile Arg Gly Gly Ala Ser | |
| 52 | 35 40 45 | |
| 53 | ttt gtg aca ggc gag cca acg tat caa gat ggc aat gga cac ggc acg | 525 |
| 54 | Phe Val Thr Gly Glu Pro Thr Tyr Gln Asp Gly Asn Gly His Gly Thr | |
| 55 | 50 55 60 | |
| 56 | cat gtg gca ggg acg att gcc gct tta aac aat tcg att ggc gtc ctt | 573 |
| 57 | His Val Ala Gly Thr Ile Ala Ala Leu Asn Asn Ser Ile Gly Val Leu | |
| 58 | 65 70 75 80 | |
| 59 | ggc gta gcg cct aat gct gaa cta tac gct gtt aaa gta tta gca gcc | 621 |
| 60 | Gly Val Ala Pro Asn Ala Glu Leu Tyr Ala Val Lys Val Leu Ala Ala | |
| 61 | 85 90 95 | |
| 62 | aac ggc aga ggc cca gtc agc tca att gcc caa ggg ttg gaa tgg gca | 669 |
| 63 | Asn Gly Arg Gly Pro Val Ser Ser Ile Ala Gln Gly Leu Glu Trp Ala | |
| 64 | 100 105 110 | |
| 65 | gga aac aat ggc atg gac gtt gcc aac ttg agt tta gga agt cca tcg | 717 |
| 66 | Gly Asn Asn Gly Met Asp Val Ala Asn Leu Ser Leu Gly Ser Pro Ser | |
| 67 | 115 120 125 | |
| 68 | cca agc gca acg ctt gag caa gcg gtt aat agc gct act tct aga ggc | 765 |
| 69 | Pro Ser Ala Thr Leu Glu Gln Ala Val Asn Ser Ala Thr Ser Arg Gly | |
| 70 | 130 135 140 | |
| 71 | gtc ctt gtc gta gca gca act gga aac tca gga aca ggc tcc ctc gac | 813 |
| 72 | Val Leu Val Val Ala Ala Thr Gly Asn Ser Gly Thr Gly Ser Leu Asp | |
| 73 | 145 150 155 160 | |
| 74 | tac cca gct cgt tat gcg aac gct atg gca gtc gga gct act gac caa | 861 |
| 75 | Tyr Pro Ala Arg Tyr Ala Asn Ala Met Ala Val Gly Ala Thr Asp Gln | |
| 76 | 165 170 175 | |
| 77 | aac aac aac cgc gcc agc ttt tct cag tac gga gca ggg ctt gac att | 909 |
| 78 | Asn Asn Asn Arg Ala Ser Phe Ser Gln Tyr Gly Ala Gly Leu Asp Ile | |
| 79 | 180 185 190 | |
| 80 | gtt gcg cca ggt gta aac gtg cag agc aca tac cca ggt tca act tac | 957 |
| 81 | Val Ala Pro Gly Val Asn Val Gln Ser Thr Tyr Pro Gly Ser Thr Tyr | |
| 82 | 195 200 205 | |
| 83 | gct agc ttc aac ggt aca tcg atg gcg act cct cac gtt gtc ggt gta | 1005 |
| 84 | Ala Ser Phe Asn Gly Thr Ser Met Ala Thr Pro His Val Val Gly Val | |
| 85 | 210 215 220 | |
| 86 | gca gcc ctt gta aaa caa aaa aac cca tct tgg tcc aat gta caa atc | 1053 |
| 87 | Ala Ala Leu Val Lys Gln Lys Asn Pro Ser Trp Ser Asn Val Gln Ile | |
| 88 | 225 230 235 240 | |
| 89 | cgc aat cat cta aag aat aca gcc aca agt ttg ggt agc acg aac ttg | 1101 |
| 90 | Arg Asn His Leu Lys Asn Thr Ala Thr Ser Leu Gly Ser Thr Asn Leu | |
| 91 | 245 250 255 | |
| 92 | tat gga agc ggg ctt gtc aat gca gaa gca gca aca cgc taa | 1143 |
| 93 | Tyr Gly Ser Gly Leu Val Asn Ala Glu Ala Ala Thr Arg | |

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99 <213> ORGANISM: Bacillus clausii
100 <400> SEQUENCE: 2
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103 Ile Ser Val Ala Phe Ser Ser Ser Ile Ala Ser Ala Ala Glu Glu Ala
104 -95 -90 -85
105 Lys Glu Lys Tyr Leu Ile Gly Phe Asn Glu Gln Glu Ala Val Ser Glu
106 -80 -75 -70 -65
107 Phe Val Glu Gln Val Asp Ala Asn Asn Asp Val Ala Val Leu Ser Glu
108 -60 -55 -50
109 Glu Glu Glu Val Glu Ile Glu Leu Leu His Glu Phe Glu Thr Ile Pro
110 -45 -40 -35
111 Val Leu Ser Val Glu Leu Ser Pro Glu Asp Val Asp Thr Leu Glu Leu
112 -30 -25 -20
113 Asp Pro Ala Ile Ser Tyr Ile Glu Glu Asp Val Glu Val Ser Ile Met
114 -15 -10 -5 -1
115 Ala Gln Ser Val Pro Trp Gly Ile Ser Arg Val Gln Ala Pro Ala Ala
116 1 5 10 15
117 His Asn Arg Gly Val Thr Gly Ser Gly Val Lys Val Ala Val Leu Asp
118 20 25 30
119 Thr Gly Ile Ser Ala His Pro Asp Leu Asn Ile Arg Gly Gly Ala Ser
120 35 40 45
121 Phe Val Thr Gly Glu Pro Thr Tyr Gln Asp Gly Asn Gly His Gly Thr
122 50 55 60
123 His Val Ala Gly Thr Ile Ala Ala Leu Asn Asn Ser Ile Gly Val Leu
124 65 70 75 80
125 Gly Val Ala Pro Asn Ala Glu Leu Tyr Ala Val Lys Val Leu Ala Ala
126 85 90 95
127 Asn Gly Arg Gly Pro Val Ser Ser Ile Ala Gln Gly Leu Glu Trp Ala
128 100 105 110
129 Gly Asn Asn Gly Met Asp Val Ala Asn Leu Ser Leu Gly Ser Pro Ser
130 115 120 125
131 Pro Ser Ala Thr Leu Glu Gln Ala Val Asn Ser Ala Thr Ser Arg Gly
132 130 135 140
133 Val Leu Val Val Ala Ala Thr Gly Asn Ser Gly Thr Gly Ser Leu Asp
134 145 150 155 160
135 Tyr Pro Ala Arg Tyr Ala Asn Ala Met Ala Val Gly Ala Thr Asp Gln
136 165 170 175
137 Asn Asn Asn Arg Ala Ser Phe Ser Gln Tyr Gly Ala Gly Leu Asp Ile
138 180 185 190
139 Val Ala Pro Gly Val Asn Val Gln Ser Thr Tyr Pro Gly Ser Thr Tyr
140 195 200 205
141 Ala Ser Phe Asn Gly Thr Ser Met Ala Thr Pro His Val Val Gly Val
142 210 215 220
143 Ala Ala Leu Val Lys Gln Lys Asn Pro Ser Trp Ser Asn Val Gln Ile

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144      225      230      235      240
145      Arg Asn His Leu Lys Asn Thr Ala Thr Ser Leu Gly Ser Thr Asn Leu
146      245      250      255
147      Tyr Gly Ser Gly Leu Val Asn Ala Glu Ala Ala Thr Arg
148      260      265
150 <210> SEQ ID NO: 3
151 <211> LENGTH: 5
152 <212> TYPE: PRT
153 <213> ORGANISM: Artificial Sequence
154 <220> FEATURE:
155 <223> OTHER INFORMATION: Synthetic
156 <400> SEQUENCE: 3
157      Ala Gly Lys Ala Leu
158      1      5
160 <210> SEQ ID NO: 4
161 <211> LENGTH: 4
162 <212> TYPE: PRT
163 <213> ORGANISM: Artificial Sequence
164 <220> FEATURE:
165 <223> OTHER INFORMATION: Synthetic
166 <400> SEQUENCE: 4
167      Ala Gly Gly Leu
168      1
170 <210> SEQ ID NO: 5
171 <211> LENGTH: 29
172 <212> TYPE: DNA
173 <213> ORGANISM: Artificial Sequence
174 <220> FEATURE:
175 <223> OTHER INFORMATION: Primer
176 <400> SEQUENCE: 5
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179 <210> SEQ ID NO: 6
180 <211> LENGTH: 32
181 <212> TYPE: DNA
182 <213> ORGANISM: Artificial Sequence
183 <220> FEATURE:
184 <223> OTHER INFORMATION: Primer
185 <400> SEQUENCE: 6
186      tttggatcca tacacaaaaa aacgctgtgc cc
188 <210> SEQ ID NO: 7
189 <211> LENGTH: 29
190 <212> TYPE: DNA
191 <213> ORGANISM: Artificial Sequence
192 <220> FEATURE:
193 <223> OTHER INFORMATION: Primer
194 <400> SEQUENCE: 7
195      aatagagctc accagcttgg acaagttgg
197 <210> SEQ ID NO: 8
198 <211> LENGTH: 32

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199 <212> TYPE: DNA
200 <213> ORGANISM: Artificial Sequence
201 <220> FEATURE:
202 <223> OTHER INFORMATION: Primer
203 <400> SEQUENCE: 8
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207 <211> LENGTH: 275
208 <212> TYPE: PRT
209 <213> ORGANISM: Bacillus
210 <400> SEQUENCE: 9
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212      1              5              10              15
213      His Ser Gln Gly Tyr Thr Gly Ser Asn Val Lys Val Ala Val Ile Asp
214      20              25              30
215      Ser Gly Ile Asp Ser Ser His Pro Asp Leu Lys Val Ala Gly Gly Ala
216      35              40              45
217      Ser Met Val Pro Ser Glu Thr Asn Pro Phe Gln Asp Asn Asn Ser His
218      50              55              60
219      Gly Thr His Val Ala Gly Thr Val Ala Ala Leu Asn Asn Ser Ile Gly
220      65              70              75              80
221      Val Leu Gly Val Ala Pro Ser Ala Ser Leu Tyr Ala Val Lys Val Leu
222      85              90              95
223      Gly Ala Asp Gly Ser Gly Gln Tyr Ser Trp Ile Ile Asn Gly Ile Glu
224      100             105             110
225      Trp Ala Ile Ala Asn Asn Met Asp Val Ile Asn Met Ser Leu Gly Gly
226      115             120             125
227      Pro Ser Gly Ser Ala Ala Leu Lys Ala Ala Val Asp Lys Ala Val Ala
228      130             135             140
229      Ser Gly Val Val Val Val Ala Ala Ala Gly Asn Glu Gly Thr Ser Gly
230      145             150             155             160
231      Ser Ser Ser Thr Val Gly Tyr Pro Gly Lys Tyr Pro Ser Val Ile Ala
232      165             170             175
233      Val Gly Ala Val Asp Ser Ser Asn Gln Arg Ala Ser Phe Ser Ser Val
234      180             185             190
235      Gly Pro Glu Leu Asp Val Met Ala Pro Gly Val Ser Ile Gln Ser Thr
236      195             200             205
237      Leu Pro Gly Asn Lys Tyr Gly Ala Tyr Asn Gly Thr Ser Met Ala Ser
238      210             215             220
239      Pro His Val Ala Gly Ala Ala Ala Leu Ile Leu Ser Lys His Pro Asn
240      225             230             235             240
241      Trp Thr Asn Thr Gln Val Arg Ser Ser Leu Glu Asn Thr Thr Thr Lys
242      245             250             255
243      Leu Gly Asp Ser Phe Tyr Tyr Gly Lys Gly Leu Ile Asn Val Gln Ala
244      260             265             270
245      Ala Ala Gln
246      275

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32

VERIFICATION SUMMARY

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Input Set : N:\DA\US09931701A.raw

Output Set: N:\CRF4\08102004\I931701A.raw

L:6 M:270 C: Current Application Number differs, Wrong Format
L:22 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:22 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:0
L:22 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:0